

Exhibit A

Clean Version of The Pending Claims in U.S. Patent Application Ser. No. 09/818,990

1. (Amended) An isolated nucleic acid molecule comprising at least 2000 contiguous bases of nucleotide sequence first disclosed in SEQ ID NO: 1.
2. (Twice Amended) An isolated nucleic acid molecule comprising a nucleotide sequence that:
 - (a) encodes the amino acid sequence shown in SEQ ID NO: 2; and
 - (b) hybridizes to the nucleotide sequence of SEQ ID NO: 1 or the complement thereof under highly stringent conditions of 0.5 M NaHPO₄, 7% sodium dodecyl sulfate (SDS) and 1 mM EDTA at 65°C and washing in 0.1x SSC/0.1%SDS at 68°C.
3. An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence shown in SEQ ID NO: 2.
6. An isolated nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 1.
7. A recombinant expression vector comprising the isolated nucleic acid molecule of claim 1.
8. The recombinant expression vector of claim 7, wherein the isolated nucleic acid molecule encodes the amino acid sequence shown in SEQ ID NO:2.
9. The recombinant expression vector of claim 8, wherein the isolated nucleic acid molecule comprises the nucleotide sequence of SEQ ID NO: 1.

10. A host cell comprising the recombinant expression vector of claim 7.

Exhibit B

Marked Up Version of Amended Claims in U.S. Patent Application Ser. No. 09/818,990

1. (Amended) An isolated nucleic acid molecule comprising at least [24] 2000 contiguous bases of nucleotide sequence first disclosed in SEQ ID NO: 1.
2. (Twice Amended) An isolated nucleic acid molecule comprising a nucleotide sequence that:
 - (a) encodes the amino acid sequence shown in SEQ ID NO: 2; and
 - (b) hybridizes [under highly stringent conditions] to the nucleotide sequence of SEQ ID NO: 1 or the complement thereof under highly stringent conditions of 0.5 M NaHPO₄, 7% sodium dodecyl sulfate (SDS) and 1 mM EDTA at 65°C and washing in 0.1x SSC/0.1%SDS at 68°C.
3. An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence shown in SEQ ID NO: 2.
6. An isolated nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 1.
7. A recombinant expression vector comprising the isolated nucleic acid molecule of claim 1.
8. The recombinant expression vector of claim 7, wherein the isolated nucleic acid molecule encodes the amino acid sequence shown in SEQ ID NO:2.
9. The recombinant expression vector of claim 8, wherein the isolated nucleic acid molecule comprises the nucleotide sequence of SEQ ID NO: 1.

10. A host cell comprising the recombinant expression vector of claim 7.

Exhibit C

Marked Up Version of Amended Title in U.S. Patent Application Ser. No. 09/818,990

Novel Human Muscle Proteins and Polynucleotides Encoding the Same

Query= SEQ ID NO:1
 (3963 letters)

Sequences producing significant alignments:	Score (bits)	E Value
AC024258.9.1.160658	<u>1794</u>	0.0
AL512429.14.1.11170	<u>1159</u>	0.0
AC016395.5.1.166869	<u>442</u>	e-121

>AC024258.9.1.160658
 Length = 160658

Score = 1794 bits (904), Expect = 0.0
 Identities = 904/904 (100%)
 Strand = Plus / Plus

Query: 1 atgcaagacgacagcatagaagcttctacttccatatctcagcttctaagagagagctat 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 110106 atgcaagacgacagcatagaagcttctacttccatatctcagcttctaagagagagctat 110165

Query: 61 ttagctgaaaccagacatcggggaaacaatgagaggagtcgagcggagccctcctccaac 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 110166 ttagctgaaaccagacatcggggaaacaatgagaggagtcgagcggagccctcctccaac 110225

Query: 121 ccttgccatttcggcagtccttctggggccgctgaaggaggcggaggccaagatgacctt 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 110226 ccttgccatttcggcagtccttctggggccgctgaaggaggcggaggccaagatgacctt 110285

Query: 181 ccagatctttcagcctttctgagccaagaagaattagacgaaagtgtcaatttggcaaga 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 110286 ccagatctttcagcctttctgagccaagaagaattagacgaaagtgtcaatttggcaaga 110345

Query: 241 ctggccatcaattacgaccctttggagaaggcagatgaaactcaagctagaaaaacgactt 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 110346 ctggccatcaattacgaccctttggagaaggcagatgaaactcaagctagaaaaacgactt 110405

Query: 301 tctcctgatcagatgaaacactcacctaatttaagttttgagcctaacttctgccaggat 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 110406 tctcctgatcagatgaaacactcacctaatttaagttttgagcctaacttctgccaggat 110465

Query: 361 aaccctcgaagtcccaccagctctaaagaaagccccaggaggcaaaaaggccacagtat 420
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 110466 aaccctcgaagtcccaccagctctaaagaaagccccaggaggcaaaaaggccacagtat 110525

Query: 421 tgttctgaaaccagtcacaaaaaagtatttttaataaggctgccgacttcattgaagag 480
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 Sbjct: 110526 tgttctgaaaccagtcacaaaaaagtatttttaataaggctgccgacttcattgaagag 110585

Query: 481 ctatcctcccttttcaaataccacagctccaaaaggattagacctcgtgcctgcaaaaac 540
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Sbjct: 110586 ctatcctcccttttcaaataccacagctccaaaaggattagacctcgtgcctgcaaaaac 110645

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Sbjct: 110646 cacaagagtaaactggaatctcaaaacaaagttatgcaggaaaacagctccagtttctca 110705

Query: 601 gatctgtcagaaagacgagaaagatcttctgttcccatccctatccctgcggataaccagg 660
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Sbjct: 110706 gatctgtcagaaagacgagaaagatcttctgttcccatccctatccctgcggataaccagg 110765

Query: 661 gataatgaagtgaatcacgccctggaacagcaggaagccaagaggcgtgaagcggagcag 720
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Sbjct: 110766 gataatgaagtgaatcacgccctggaacagcaggaagccaagaggcgtgaagcggagcag 110825

Query: 721 gctgccagtgaaggcggtggtggagacactacaccagggtcttcccttcatctctgtac 780
|||||
Sbjct: 110826 gctgccagtgaaggcggtggtggagacactacaccagggtcttcccttcatctctgtac 110885

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|||||
Sbjct: 110886 tatgaagaacctctggggcaacctccccgggttcaactcaaaagttacggagcagagaagtt 110945

Query: 841 ccagaaggaactcgagtacagttggattgcatagtggtaggaattccaccacctcaagta 900
|||||
Sbjct: 110946 ccagaaggaactcgagtacagttggattgcatagtggtaggaattccaccacctcaagta 111005

Query: 901 aggt 904
||||
Sbjct: 111006 aggt 111009

Score = 728 bits (367), Expect = 0.0
Identities = 372/375 (99%)
Strand = Plus / Plus

Query: 1599 aggaaatgaggacctcagcaacaacgggtctcttcaactcagccaactcyaccaccaacct 1658
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Sbjct: 154959 aggaaatgaggacctcagcaacaacgggtctcttcaactcagccaactctaccaccaacct 155018

Query: 1659 ggcagctattgagccacagccctccccaccccaactcagagcctccatctgtggaacaacc 1718
|||||
Sbjct: 155019 ggcagctattgagccacagccctccccaccccaactcagagcctccatctgtggaacaacc 155078

Query: 1719 ccccaaaccctcgaggggttctggtgaaccacaatgagccccggtccagctccag 1778
 |||
 Sbjct: 155079 ccccaaaccctcgaggggttctggtgaaccacaatgagccccggtccagctccag 155138

Query: 1779 gattgggcttcgtgtgcacttcaacctgcctgaagatgacaaaggaagtgaagcatcctc 1838
 |||
 Sbjct: 155139 gattgggcttcgtgtgcacttcaacctgcctgaagatgacaaaggaagtgaagcatcctc 155198

Query: 1839 cgaggctggtgtggtgaccaccagacagaccaggccccgattctttscaggagaggttcaa 1898
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 Sbjct: 155199 cgaggctggtgtggtgaccaccagacagaccaggccccgattctttccaggagaggttcaa 155258

Query: 1899 cggacaggcaacaaaaaccccagagccttctttccccgtgaaagagccccctccagttct 1958
 |||
 Sbjct: 155259 cggacaggcaacaaaaaccccagagccttctttccccgtgaaagagccccctccagttct 155318

Query: 1959 ggccaaaccctaaact 1973
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 Sbjct: 155319 ggccaaaccctaaact 155333

Score = 355 bits (179), Expect = 1e-94
 Identities = 179/179 (100%)
 Strand = Plus / Plus

Query: 901 aggtggtactgtgaaggcaaggagcttgaaaattccccagatattcacatcgtccaggca 960
 |||
 Sbjct: 131605 aggtggtactgtgaaggcaaggagcttgaaaattccccagatattcacatcgtccaggca 131664

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 Sbjct: 131665 ggaaatctgcactcactgaccattgcggaagcctttgaagaggacacaggacgctattcc 131724

Query: 1021 tgctttgcttctaacaatctatgggacagattcgacttctgctgagatttatatagaagg 1079
 |||
 Sbjct: 131725 tgctttgcttctaacaatctatgggacagattcgacttctgctgagatttatatagaagg 131783

Score = 286 bits (144), Expect = 9e-74
 Identities = 144/144 (100%)
 Strand = Plus / Plus

Query: 1316 agatgctacaaaatttgtcagcttctgagggtcagctggttgtctttgaatgcagagtaa 1375
 |||
 Sbjct: 147151 agatgctacaaaatttgtcagcttctgagggtcagctggttgtctttgaatgcagagtaa 147210

Query: 1376 aaggagctccatctcctaagggttgagtggatatagagaagggactttaatagaagattctc 1435
|||||
Sbjct: 147211 aaggagctccatctcctaagggttgagtggatatagagaagggactttaatagaagattctc 147270

Query: 1436 cagattttaggattttacagaaaa 1459
|||||
Sbjct: 147271 cagattttaggattttacagaaaa 147294

Score = 238 bits (120), Expect = 2e-59
Identities = 120/120 (100%)
Strand = Plus / Plus

Query: 1482 agaggagatttgacaccttggtcattgctgaggtgttgacagaagattctgggtgcttcac 1541
|||||
Sbjct: 154367 agaggagatttgacaccttggtcattgctgaggtgttgacagaagattctgggtgcttcac 154426

Query: 1542 atgtactgcaagcaacaatacggcacagtgtcaagcattgcacagctgcacgtgagagg 1601
|||||
Sbjct: 154427 atgtactgcaagcaacaatacggcacagtgtcaagcattgcacagctgcacgtgagagg 154486

Score = 230 bits (116), Expect = 5e-57
Identities = 116/116 (100%)
Strand = Plus / Plus

Query: 1130 gaatccagaagccaaatgaggtgtcatctcctcccactacctctgcagtcattcctccag 1189
|||||
Sbjct: 137019 gaatccagaagccaaatgaggtgtcatctcctcccactacctctgcagtcattcctccag 137078

Query: 1190 cagtaccccaagcccagcatttggtggcccaacctcggtggcaaccatccagcag 1245
|||||
Sbjct: 137079 cagtaccccaagcccagcatttggtggcccaacctcggtggcaaccatccagcag 137134

Score = 149 bits (75), Expect = 1e-32
Identities = 75/75 (100%)
Strand = Plus / Plus

Query: 1243 cagtgtcagagccccaccaattacttgagggttgatggaaaacctatcattgcagct 1302
|||||
Sbjct: 138704 cagtgtcagagccccaccaattacttgagggttgatggaaaacctatcattgcagct 138763

Query: 1303 cctgtgtttacaaag 1317
|||||
Sbjct: 138764 cctgtgtttacaaag 138778

Score = 107 bits (54), Expect = 5e-20
Identities = 54/54 (100%)
Strand = Plus / Plus

Query: 1077 agggggtttcttcttctgactcagaaggcgaccctaacaaggaagagatgaatcg 1130
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Sbjct: 134140 agggggtttcttcttctgactcagaaggcgaccctaacaaggaagagatgaatcg 134193

Score = 48.1 bits (24), Expect = 0.041
Identities = 24/24 (100%)
Strand = Plus / Plus

Query: 1460 aacctcgatccatggcagagccag 1483
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Sbjct: 150396 aacctcgatccatggcagagccag 150419

>AL512429.14.1.11170
Length = 11170

Score = 1159 bits (584), Expect = 0.0
Identities = 588/592 (99%)
Strand = Plus / Plus

Query: 1974 tgattccactcagttacaacagcttcataaccaagtcttactggaacaacaccaattgca 2033
|||||
Sbjct: 4075 tgattccactcagttacaacagcttcataaccaagtcttactggaacaacaccaattgca 4134

Query: 2034 aaaccacctccttcattctcctaaggagtttctttcarcatgactgttttgaactccaa 2093
|||||
Sbjct: 4135 aaaccacctccttcattctcctaaggagtttctttcagcatgactgttttgaactccaa 4194

Query: 2094 tgctccccccagcggtgacaacatccartaagcaggtgaaggctccttcattcacagacgtt 2153
|||||
Sbjct: 4195 tgctccccccagcggtgacaacatccagtaagcaggtgaaggctccttcattcacagacgtt 4254

Query: 2154 cagcttggcccgccgaagtatttcttccctccacgaacaccaccgcagcaactgtggc 2213
|||||
Sbjct: 4255 cagcttggcccgccgaagtatttcttccctccacgaacaccaccgcagcaactgtggc 4314

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|||||
Sbjct: 4315 cccttccagctctccggtgttcactttgagcagcactcctcaaactattcagaggacagt 4374

Query: 2274 gagcaaagaaagcctcttagtggtctcaccctctgtgcaaaccaaatctccaggagggt 2333
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Sbjct: 4375 gagcaaagaaagcctcttagtggtctcaccctctgtgcaaaccaaatctccaggagggt 4434

Query: 2334 ttccatccaaaatgagccactcccaccaggcccaacagaacccracaccaccaccattcac 2393
|||||
Sbjct: 4435 ttccatccaaaatgagccactcccaccaggcccaacagaacccracaccaccaccattcac 4494

Query: 2394 attttccatccccagcggaaccagtttcagccccgctgtgtgtccccaattcctgtctc 2453
|||||
Sbjct: 4495 attttccatccccagcggaaccagtttcagccccgctgtgtgtccccaattcctgtctc 4554

Query: 2454 tcctaccagccggattcagaaccagtggtttcctcagctctgttctgccttctctccc 2513
|||||
Sbjct: 4555 tcctaccagccggattcagaaccagtggtttcctcagctctgttctgccttctctccc 4614

Query: 2514 tgccatcccacccacaaatgccatgggrgtgcctagaagtgcaccatccatg 2565
|||||
Sbjct: 4615 tgccatcccacccacaaatgccatgggggtgcctagaagtgcaccatccatg 4666

Score = 278 bits (140), Expect = 2e-71
Identities = 140/140 (100%)
Strand = Plus / Plus

Query: 2565 gccatcccagggattagcgaagaaaaatacaaagtctcctcaaccagtgaatgatgataa 2624
|||||
Sbjct: 5332 gccatcccagggattagcgaagaaaaatacaaagtctcctcaaccagtgaatgatgataa 5391

Query: 2625 cattcgtgaaactaagaacgcagtgattcgagacttggggaaaaaaataacttttcagtga 2684
|||||
Sbjct: 5392 cattcgtgaaactaagaacgcagtgattcgagacttggggaaaaaaataacttttcagtga 5451

Query: 2685 tgtcagaccaaaccagcagg 2704
|||||
Sbjct: 5452 tgtcagaccaaaccagcagg 5471

>AC016395.5.1.166869
Length = 166869

Score = 442 bits (223), Expect = e-121
Identities = 226/227 (99%)
Strand = Plus / Minus

Query: 2701 caggagtacaaaatttcaagctttgagcagaggctgatgaatgaaatagagtttcgcttg 2760
|||||
Sbjct: 157129 caggagtacaaaatttcaagctttgagcagaggctgatgaatgaaatagagtttcgcttg 157070

Query: 2761 gaacgtactcctgttgatgaatcagatgatgaaattcaacatgatgagatccccacgggc 2820
|||||
Sbjct: 157069 gaacgtactcctgttgatgaatcagatgatgaaattcaacatgatgagatccccacgggc 157010

Query: 2821 aagtgtattgctcccatctttgacaagagactcaagcacttccgggtcacagaaggctct 2880
|||||
Sbjct: 157009 aagtgtattgctcccatctttgacaagagactcaagcacttccgggtcacagaaggctct 156950

Query: 2881 ccagtcacattcacctgcaaaattggtgggatacctgttccaaaggt 2927
|||||
Sbjct: 156949 ccagttacattcacctgcaaaattggtgggatacctgttccaaaggt 156903

Score = 417 bits (210), Expect = e-113
Identities = 210/210 (100%)
Strand = Plus / Minus

Query: 3284 aggtgagtgggtttaccgcccccgagctgacatggctactcaatggccaacctgtgctac 3343
|||||
Sbjct: 146665 aggtgagtgggtttaccgcccccgagctgacatggctactcaatggccaacctgtgctac 146606

Query: 3344 cagatgcctcccacaagatgctgggtcagggagaccggagtccactctctgctcattgacc 3403
|||||
Sbjct: 146605 cagatgcctcccacaagatgctgggtcagggagaccggagtccactctctgctcattgacc 146546

Query: 3404 cactcactcagcgcgacgcagggacctataagtgcacgctaccaacaaaaccgggcaga 3463
|||||
Sbjct: 146545 cactcactcagcgcgacgcagggacctataagtgcacgctaccaacaaaaccgggcaga 146486

Query: 3464 attcttttagtctggagctctctgtagtag 3493
|||||
Sbjct: 146485 attcttttagtctggagctctctgtagtag 146456

Score = 339 bits (171), Expect = 6e-90
Identities = 171/171 (100%)
Strand = Plus / Minus

Query: 3793 gctcagtggcaccatcagatcccaccgcccagtgctgtccggcccagtggcagtcgctac 3852
|||||
Sbjct: 135746 gctcagtggcaccatcagatcccaccgcccagtgctgtccggcccagtggcagtcgctac 135687

Query: 3853 ggatctctcaccagtaaaggacttgacatattttctgccttttctccatggaaagcacg 3912
|||||
Sbjct: 135686 ggatctctcaccagtaaaggacttgacatattttctgccttttctccatggaaagcacg 135627

Query: 3913 atggtgtattcatgctcttctcggagtgtagtggagagtgatgaacttta 3963
|||||
Sbjct: 135626 atggtgtattcatgctcttctcggagtgtagtggagagtgatgaacttta 135576

Score = 333 bits (168), Expect = 4e-88
Identities = 168/168 (100%)
Strand = Plus / Minus

Query: 3492 agccaaagaggtgaagaaagcacctgtgatcctggagaaactacagaactgcggtgttcc 3551
|||||
Sbjct: 144204 agccaaagaggtgaagaaagcacctgtgatcctggagaaactacagaactgcggtgttcc 144145

Query: 3552 cgaaggccaccccgtagactggagtgccgcgtgataggcatgccccacctgtgttcta 3611
|||||
Sbjct: 144144 cgaaggccaccccgtagactggagtgccgcgtgataggcatgccccacctgtgttcta 144085

Query: 3612 ctggaagaaagacaatgagaccatcccttgaccagagagaggatcag 3659
|||||
Sbjct: 144084 ctggaagaaagacaatgagaccatcccttgaccagagagaggatcag 144037

Score = 306 bits (154), Expect = 9e-80
Identities = 158/159 (99%), Gaps = 1/159 (0%)
Strand = Plus / Minus

Query: 2924 aggtttactggttcaaagatgggaagcagatttctaagagaaatgagcactgcaaaatga 2983
|||||
Sbjct: 151670 aggtttactggttcaaagatgggaagcagatttctaagagaaatgagcactgcaaaatga 151611

Query: 2984 ggcgagaaggagatgggacatgctctctgcacattgaatccactaccagtgatgacgatg 3043
|||||
Sbjct: 151610 ggcgagaaggagatgggacatgctctctgcacattgaatccactaccagtgatgacgatg 151551

Query: 3044 gcaactacaccatcatggcagccaacccccagg-ggaga 3081
|||||
Sbjct: 151550 gcaactacaccatcatggcagccaacccccagggtggaga 151512

Score = 272 bits (137), Expect = 1e-69
Identities = 137/137 (100%)
Strand = Plus / Minus

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|||||
Sbjct: 139264 cagtatgcaccaggacacaacagggatgcctgccttctcattcagccagccaagaaatc 139205

Query: 3717 agacgctggatggtacacgttgtcagccaagaatgaagccggcatcgtgtcgtgcactgc 3776
|||||
Sbjct: 139204 agacgctggatggtacacgttgtcagccaagaatgaagccggcatcgtgtcgtgcactgc 139145

Query: 3777 caggctggatatatacg 3793
|||||
Sbjct: 139144 caggctggatatatacg 139128

Score = 260 bits (131), Expect = 5e-66
Identities = 131/131 (100%)
Strand = Plus / Minus

Query: 3157 aggggaagatcccgagtgaagaaagagacaaagagcccctacaggaacgctttttccga 3216
|||||
Sbjct: 148681 aggggaagatcccgagtgaagaaagagacaaagagcccctacaggaacgctttttccga 148622

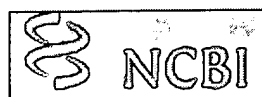
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|||||
Sbjct: 148621 ccacatttcctgcaggctcctggggatattggtagctcatgaggggagcctctgtcggctg 148562

Query: 3277 gactgtaaggt 3287
|||||
Sbjct: 148561 gactgtaaggt 148551

Score = 173 bits (87), Expect = 1e-39
Identities = 87/87 (100%)
Strand = Plus / Minus

Query: 3073 caggggagaatcagctgttctggccacttgatgggtacaaagtttgcccattcgagtcgg 3132
|||||
Sbjct: 150584 caggggagaatcagctgttctggccacttgatgggtacaaagtttgcccattcgagtcgg 150525

Query: 3133 ctaacctctgctgggtcagtctcacagg 3159
|||||
Sbjct: 150524 ctaacctctgctgggtcagtctcacagg 150498



Nucleotide

PubMed

Nucleotide

Protein

Genome

Structure

PMC

Taxonomy

OMIM

Boo

Search for

Clear

card

Limits

[Preview/Index](#)

History

Clipboard

Details

Display

default

Show:

20

Send to

File

Get Subsequence

□ 1: AL512429. Human DNA sequenc...[gi:16508239]

Links

```

LOCUS       AL512429          11170 bp      DNA          linear      PRI 26-OCT-2001
DEFINITION  Human DNA sequence from clone RP11-429C3 on chromosome 10, complete
sequence.
ACCESSION   AL512429
VERSION     AL512429.14   GI:16508239
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 11170)
  AUTHORS   Mashreghi-Mohammadi,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
            requests: clonerequest@sanger.ac.uk
COMMENT     On Oct 29, 2001 this sequence version replaced gi:15028699.
            During sequence assembly data is compared from overlapping clones.
            Where differences are found these are annotated as variations
            together with a note of the overlapping clone name. Note that the
            variation annotation may not be found in the sequence submission
            corresponding to the overlapping clone, as we submit sequences with
            only a small overlap as described above.
            This sequence was finished as follows unless otherwise noted: all
            regions were either double-stranded or sequenced with an alternate
            chemistry or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by at least
            one plasmid subclone or more than one M13 subclone; and the
            assembly was confirmed by restriction digest. The following
            abbreviations are used to associate primary accession numbers given
            in the feature table with their source databases: Em:, EMBL; Sw:,
            SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
            database can be found at
            http://www.sanger.ac.uk/Projects/C\_elegans/wormpep This sequence
            was generated from part of bacterial clone contigs of human
            chromosome 10, constructed by the Sanger Centre Chromosome 10
            Mapping Group. Further information can be found at
            http://www.sanger.ac.uk/HGP/Chr10
            RP11-429C3 is from the library RPCI-11.2 constructed by the group
            of Pieter de Jong. For further details see
            http://www.chori.org/bacpac/home.htm
            VECTOR: pBACe3.6
            IMPORTANT: This sequence is not the entire insert of clone
            RP11-429C3 It may be shorter because we sequence overlapping
            sections only once, except for a short overlap.
            The true left end of clone RP11-153K11 is at 9171 in this sequence.

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Genome

Structure

PMC

Taxonomy

OMIM

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☐ 1: AC016395. Homo sapiens chro...[gi:20564406]

Links

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AUTHORS Smith,D.R.
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Sequence Data
JOURNAL Unpublished
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AUTHORS Smith,D.R.
TITLE Direct Submission
JOURNAL Submitted (26-NOV-1999) Genome Therapeutics Corporation, 100 Beaver
Street, Waltham, MA 02453, USA
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COMMENT On May 14, 2002 this sequence version replaced gi:9929646.
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AUTHORS Bang, M.L., Mudry, R.E., McElhinny, A.S., Trombitas, K., Geach, A.J.,
Yamasaki, R., Sorimachi, H., Granzier, H., Gregorio, C.C. and Labeit, S.
TITLE Myopalladin, a novel 145-kilodalton sarcomeric protein with
multiple roles in Z-disc and I-band protein assemblies
JOURNAL J. Cell Biol. 153 (2), 413-427 (2001)
MEDLINE 21206024
PUBMED 11309420
REFERENCE 2 (bases 1 to 5707)
AUTHORS Bang, M.-L.
TITLE Direct Submission
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European Molecular Biology Laboratory (EMBL), Meyerhofstrasse 1,
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5641 cctagaagag tacctagcac aaagtagaca ttcaataaat atttgctggt tgaatgaaaa
5701 aaaaaaa
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